

SEQUENCE LISTING

<110> Gross, Jane A.
Xu, Wenfeng
Madden, Karen
Yee, David P.

<120> SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING

<130> 98-75

<150> 60/115,068
<151> 1999-01-07

<150> 60/169,890
<151> 1999-12-09

<160> 60

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 1192
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (6)...(746)

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Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val
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gac cag gag gag cgc tgg tca ctc agc tgc cgc aag gag caa ggc aag 98
Asp Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys
20 25 30

ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt 146
Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys
35 40 45

gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg	194
50 55 60	
agc cca gtg aac ctt cca cca gag ctc agg aga cag cg ^g agt gga gaa Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu	242
65 70 75	
gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag cac Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His	290
80 85 90 95	
aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala	338
100 105 110	
gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt gcc Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala	386
115 120 125	
gtc ctc tgc tgc ttc ctg gtg gc ^g gtg gcc tgc ttc ctc aag aag agg Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg	434
130 135 140	
ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt ccg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro	482
145 150 155	
gcc aag tct tcc cag gat cac gc ^g atg gaa gcc ggc agc cct gtg agc Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser	530
160 165 170 175	
aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag tgc Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys	578
180 185 190	
agg gc ^g ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac ccc Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro	626
195 200 205	
act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg cag Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln	674
210 215 220	

cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg cct 722
 Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro
 225 230 235

gcc cag gag ggg ggc cca ggt gca taaatgggg tcagggaggg aaaggaggag 776
 Ala Gln Glu Gly Gly Pro Gly Ala
 240 245

ggagagagat ggagaggagg ggagagagaa agagaggtgg ggagagggga gagagatatg 836
 aggagagaga gacagaggag gcagagaggg agagaaaacag aggagacaga gagggagaga 896
 gagacagagg gagagagaga cagagggaa gagaggcaga gagggaaaaga ggcagagaag 956
 gaaagaggca gagagggaga gaggcagaga gggagagagg cagagagaca gagagggaga 1016
 gagggacaga gagagataga gcaggaggc ggggactct gagtcccagt tcccagtgc 1076
 gctgttaggtc gtcacacact aaccacacgt gcaataaaagt cctcgtgcct gtcgtcaca 1136
 gcccccgaga gccctccctc ctggagaata aaacctttgg cagctgcct tccta 1192

<210> 2

<211> 247

<212> PRT

<213> Homo sapiens

<400> 2

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
 1 5 10 15
 Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
 20 25 30
 Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
 35 40 45
 Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
 50 55 60
 Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
 65 70 75 80
 Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg
 85 90 95
 Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp
 100 105 110
 Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val
 115 120 125
 Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly
 130 135 140
 Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala
 145 150 155 160
 Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr
 165 170 175
 Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg

180	185	190
Ala Pro Thr Gln Glu Ser Ala Val	Thr Pro Gly Thr Pro Asp Pro Thr	
195	200	205
Cys Ala Gly Arg Trp Gly Cys His	Thr Arg Thr Thr Val Leu Gln Pro	
210	215	220
Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala		
225	230	235
Gln Glu Gly Gly Pro Gly Ala		240
	245	

<210> 3
<211> 360
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(360)

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cag gag gag cgc tgg tca ctc agc tgc cgc aag gag caa ggc aag ttc Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe 20 25 30	96
tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt gga Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly 35 40 45	144
cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg agc Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser 50 55 60	192
cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa gtt Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val 65 70 75 80	240
gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag cac aga Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg 85 90 95	288
ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca gat	336

Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp
 100 105 110

cag gtg gcc ctg gtc tac agc acg 360
 Gln Val Ala Leu Val Tyr Ser Thr
 115 120

<210> 4
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
 1 5 10 15
 Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
 20 25 30
 Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
 35 40 45
 Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
 50 55 60
 Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
 65 70 75 80
 Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg
 85 90 95
 Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp
 100 105 110
 Gln Val Ala Leu Val Tyr Ser Thr
 115 120

<210> 5
 <211> 1377
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (14)...(895)

<400> 5 49
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 Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg
 1 5 10

agc cgt gtg gac cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly	97
15 20 25	
gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu	145
30 35 40	
ggt acc tgc atg tcc tgc aaa acc att tgc aac cat cag agc cag cgc Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg	193
45 50 55 60	
acc tgt gca gcc ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly	241
65 70 75	
aag ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile	289
80 85 90	
tgt gga cag cac cct aagcaa tgt gca tac ttc tgt gag aac aag ctc Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu	337
95 100 105	
agg agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly	385
110 115 120	
gaa gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag Glu Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu	433
125 130 135 140	
cac aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser	481
145 150 155	
gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys	529
160 165 170	
gcc gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys	577
175 180 185	
agg ggg gat ccc tgc tcc cag ccc cgc tca agg ccc cgt caa agt	625

Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser			
190	195	200	
ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg			673
Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val			
205	210	215	220
agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag			721
Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu			
225	230	235	
tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac			769
Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp			
240	245	250	
ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg			817
Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu			
255	260	265	
cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg			865
Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val			
270	275	280	
cct gcc cag gag ggg ggc cca ggt gca taa atgggggtca gggagggaaa			915
Pro Ala Gln Glu Gly Gly Pro Gly Ala *			
285	290		
ggaggagggagagatgga gagaggggagagagaaaga gaggtggggagagag			975
agatatgagg agagagagac agaggaggca gaaaggaga gaaacagagg agacagagag			1035
ggagagagag acagagggag agagagacag agggaaagag aggcagagag ggaaagaggc			1095
agagaaggaa agagacagggc agagaaggag agaggcagag agggagagag gcagagaggg			1155
agagaggcag agagacagag agggagagag ggacagagag agatagagca ggaggtcggt			1215
gcactctgag tcccagttcc cagtgcagct gtaggtcgtc atcacctaac cacacgtca			1275
ataaagtctt cgtgcctgct gctcacagcc cccgagagcc cctcctcctg gagaataaaa			1335
cctttggcag ctgcccttcc taaaaaaaaaaaaaa aa			1377

<210> 6

<211> 293

<212> PRT

<213> Homo sapiens

<400> 6

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp			
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Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg			

20	25	30
Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met		
35	40	45
Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala		
50	55	60
Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp		
65	70	75
His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His		
85	90	95
Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val		
100	105	110
Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn		
115	120	125
Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser		
130	135	140
Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val		
145	150	155
Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys		
165	170	175
Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro		
180	185	190
Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser		
195	200	205
Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro		
210	215	220
Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro		
225	230	235
Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala		
245	250	255
Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro		
260	265	270
His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu		
275	280	285
Gly Gly Pro Gly Ala		
290		

<210> 7

<211> 995

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (219)...(773)

<400> 7

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agctgctctt gctgcatttg ctctggaatt ctgttagaga tattacttgt cttccaggc		180
tgttcttctt gtagctccct tttttcttt ttgtgatc atg ttg cag atg gct ggg		236
	Met Leu Gln Met Ala Gly	
	1 5	
cag tgc tcc caa aat gaa tat ttt gac agt ttg ttg cat gct tgc ata		284
Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu Leu His Ala Cys Ile		
10 15 20		
cct tgt caa ctt cga tgt tct aat act cct cct cta aca tgt cag		332
Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln		
25 30 35		
cgt tat tgt aat gca agt gtg acc aat tca gtg aaa gga acg aat gcg		380
Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val Lys Gly Thr Asn Ala		
40 45 50		
att ctc tgg acc tgt ttg gga ctg agc tta ata att tct ttg gca gtt		428
Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu Ile Ile Ser Leu Ala Val		
55 60 65 70		
ttc gtg cta atg ttt ttg cta agg aag ata agc tct gaa cca tta aag		476
Phe Val Leu Met Phe Leu Leu Arg Lys Ile Ser Ser Glu Pro Leu Lys		
75 80 85		
gac gag ttt aaa aac aca gga tca ggt ctc ctg ggc atg gct aac att		524
Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu Leu Gly Met Ala Asn Ile		
90 95 100		
gac ctg gaa aag agc agg act ggt gat gaa att att ctt ccg aga ggc		572
Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu Ile Ile Leu Pro Arg Gly		
105 110 115		
ctc gag tac acg gtg gaa gaa tgc acc tgt gaa gac tgc atc aag agc		620
Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys Glu Asp Cys Ile Lys Ser		
120 125 130		
aaa ccg aag gtc gac tct gac cat tgc ttt cca ctc cca gct atg gag		668
Lys Pro Lys Val Asp Ser Asp His Cys Phe Pro Leu Pro Ala Met Glu		
135 140 145 150		
gaa ggc gca acc att ctt gtc acc acg aaa acg aat gac tat tgc aag		716

Glu Gly Ala Thr Ile Leu Val Thr Thr Lys Thr Asn Asp Tyr Cys Lys
 155 160 165
 agc ctg cca gct gct ttg agt gct acg gag ata gag aaa tca att tct 764
 Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu Ile Glu Lys Ser Ile Ser
 170 175 180
 gct agg taa ttaaccattt cgactcgagc agtgccactt taaaaatctt 813
 Ala Arg *

 ttgtcagaat agatgatgtg tcagatctct ttaggatgac tgtatTTTC agttGCCGAT 873
 acagCTTTT gtcctctaAC tgtggAAACT cTTTATGTTA gatATATTc TCTAGGTTAC 933
 tgTTGGGAGC tTAATGGTAG aaACTTCCTT ggTTTCAcGA tTAAAGTCTT TTTTTTCCT 993
 ga 995

 <210> 8
 <211> 184
 <212> PRT
 <213> Homo sapiens

 <400> 8
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 Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
 20 25 30
 Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
 35 40 45
 Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu
 50 55 60
 Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile
 65 70 75 80
 Ser Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu
 85 90 95
 Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu
 100 105 110
 Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys
 115 120 125
 Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
 130 135 140
 Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys
 145 150 155 160
 Thr Asn Asp Tyr Cys Lys Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu
 165 170 175
 Ile Glu Lys Ser Ile Ser Ala Arg

180

<210> 9
 <211> 245
 <212> PRT
 <213> Homo sapiens

<400> 9

Gly	Arg	Ser	Arg	Arg	Gly	Gly	Arg	Ser	Arg	Val	Asp	Gln	Glu	Glu	Arg
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Phe	Pro	Gln	Gly	Leu	Trp	Thr	Gly	Val	Ala	Met	Arg	Ser	Cys	Pro	Glu
				20				25				30			
Glu	Gln	Tyr	Trp	Asp	Pro	Leu	Leu	Gly	Thr	Cys	Met	Ser	Cys	Lys	Thr
				35				40			45				
Ile	Cys	Asn	His	Gln	Ser	Gln	Arg	Thr	Cys	Ala	Ala	Phe	Cys	Arg	Ser
				50				55			60				
Leu	Ser	Cys	Arg	Lys	Glu	Gln	Gly	Lys	Phe	Tyr	Asp	His	Leu	Leu	Arg
				65				70			75		80		
Asp	Cys	Ile	Ser	Cys	Ala	Ser	Ile	Cys	Gly	Gln	His	Pro	Lys	Gln	Cys
				85				90			95				
Ala	Tyr	Phe	Cys	Glu	Asn	Lys	Leu	Arg	Ser	Pro	Val	Asn	Leu	Pro	Pro
				100				105			110				
Glu	Leu	Arg	Arg	Gln	Arg	Ser	Gly	Glu	Val	Glu	Asn	Ser	Asp	Asn	
				115				120			125				
Ser	Gly	Arg	Tyr	Gln	Gly	Leu	Glu	His	Arg	Gly	Ser	Glu	Ala	Ser	Pro
				130				135			140				
Ala	Leu	Pro	Gly	Leu	Lys	Leu	Ser	Ala	Asp	Gln	Val	Ala	Leu	Val	Tyr
				145				150			155		160		
Ser	Thr	Leu	Gly	Leu	Cys	Leu	Cys	Ala	Val	Leu	Cys	Cys	Phe	Leu	Val
				165				170			175				
Ala	Val	Ala	Cys	Phe	Leu	Lys	Lys	Arg	Gly	Asp	Pro	Cys	Ser	Cys	Gln
				180				185			190				
Pro	Arg	Ser	Arg	Pro	Arg	Gln	Ser	Pro	Ala	Lys	Ser	Ser	Gln	Asp	His
				195				200			205				
Ala	Met	Glu	Ala	Gly	Ser	Pro	Val	Ser	Thr	Ser	Pro	Glu	Pro	Val	Glu
				210				215			220				
Thr	Cys	Ser	Phe	Cys	Phe	Pro	Glu	Cys	Arg	Ala	Pro	Thr	Gln	Glu	Ser
				225				230			235		240		
Ala	Val	Thr	Pro	Gly											
				245											

<210> 10
 <211> 40
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Motif describing the cysteine-rich pseudo-repeat domain

<221> VARIANT

<222> (1)...(2)

<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

<221> VARIANT

<222> (4)...(4)

<223> Xaa is any amino acid residue except cysteine.

<221> VARIANT

<222> (5)...(5)

<223> Xaa is glutamine, glutamic acid, or lysine.

<221> VARIANT

<222> (6)...(6)

<223> Xaa is glutamine, glutamic acid, lysine, asparagine, arginine, aspartic acid, histidine, or serine.

<221> VARIANT

<222> (7)...(7)

<223> Xaa is glutamine or glutamic acid.

<221> VARIANT

<222> (8)...(9)

<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

<221> VARIANT

<222> (10)...(11)

<223> Xaa is tyrosine, phenylalanine, or tryptophan.

<221> VARIANT

<222> (13)...(13)

<223> Xaa is any amino acid residue except cysteine.

<221> VARIANT

<222> (16)...(17)

<223> Each Xaa is independently any amino acid residue

except cysteine.

<221> VARIANT

<222> (19) . . . (19)

<223> Xaa is isoleucine, methionine, leucine, or valine.

<221> VARIANT

<222> (20) . . . (20)

<223> Xaa is any amino acid residue except cysteine.

<221> VARIANT

<222> (??) (24)

<223> Each Xaa is independently any amino acid residue except cysteine.

<221> VARTANT

<222> (26) (31)

<223> Each Xaa is independently any amino acid residue except cysteine

<221> VARIANT

<222> (32) (33)

<222> Each Xaa is independently any amino acid residue except cysteine or absent

<221> VARTANT

<221> VARIANT
<222> (35) (36)

<222> Each Xaa is independently any amino acid residue except cysteine

<221> VARTANT

<222> VARIANT

<223> Xaa is tyrosine or phenylalanine

<221> VARTANT

<222> (39) (40)

<222> (33)....(40)
<223> Each Xaa is independently any amino acid residue except cysteine or absent

<400> 10

-400- 10
Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Leu Leu Xaa
1 5 10 15
Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa

35

40

<210> 11
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide sequence encoding the polypeptide of SEQ ID NO:4

<221> variation
 <222> (1)...(360)
 <223> Each N is independently A, T, G, or C.

<400> 11

atgwsngny tnggnmgnws nmgnmgnngn ggnmgnwsnm gngtngayca rgargarmgn	60
tggwsnytnw sntgymgnaa rgarcarggn aarttytayg aycaytnty nmgngaytgy	120
athwsntgyg cnwsnathtg yggncarcay ccnaarcart gygcntaytt ytgygaraay	180
aarytnmgnw snccngtnaa yytnccnccn garytnmgnm gncarmgnws nggngargtn	240
garaayaayw sngayaayws nggnmgnay carggnytng arcaymgnng nwsngargcn	300
wsnccngcny tnccngnyt naarytnwsn gcngaycarg tngcnytngt ntaywsnacn	360

<210> 12
 <211> 741
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide sequence encoding a polypeptide of SEQ ID NO:2

<221> variation
 <222> (1)...(741)
 <223> Each N is independently A, T, G, or C.

<400> 12

atgwsngny tnggnmgnws nmgnmgnngn ggnmgnwsnm gngtngayca rgargarmgn	60
tggwsnytnw sntgymgnaa rgarcarggn aarttytayg aycaytnty nmgngaytgy	120
athwsntgyg cnwsnathtg yggncarcay ccnaarcart gygcntaytt ytgygaraay	180
aarytnmgnw snccngtnaa yytnccnccn garytnmgnm gncarmgnws nggngargtn	240
garaayaayw sngayaayws nggnmgnay carggnytng arcaymgnng nwsngargcn	300
wsnccngcny tnccngnyt naarytnwsn gcngaycarg tngcnytngt ntaywsnacn	360
ytnggnytnt gyytntgygc ngtnytny tgyttytng tngcngtngc ntgyttyytn	420
aaraarmngng gngayccntg ywsntgycar ccnmgmgnwsnm gnccnmgnca rwsnccngcn	480

aarwsnwsnc argaycaygc natggargcn ggnwsnccng tnwsnacnws nccngarccn	540
gtngaracnt gywsnttytg yttyccngar tgymgngcnc cnacncarga rwsngcngtn	600
acnccnggna cnccngaycc nacntgygcn ggnmgntggg gntgycayac nmgnacnacn	660
gtnytnarc cntgyccnca yathccngay wsnggnytng gnathgtntg ygtncngcn	720
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<211> 8

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<220>

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<400> 13

Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys
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<210> 14

<211> 7

<212> PRT

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<220>

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<400> 14

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<210> 15

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC19980

<400> 15

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<210> 16

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC19981

<400> 16

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23

<210> 17

<211> 1149

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (236)...(1027)

<400> 17

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gccctgccat gtagtgcacg caggacatca acaaacacag ataacaggaa atgatccatt	120
ccctgtggtc acttattcta aaggccccaa cttcaaaagt tcaagtagtg atatggatga	180
ctccacagaa agggagcagt cacgccttac ttcttgcctt aagaaaagag aagaa atg	238
	Met
	1

aaa ctg aag gag tgg gtt tcc atc ctc cca cgg aag gaa agc ccc tct	286
Lys Leu Lys Glu Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser	
5 10 15	

gtc cga tcc tcc aaa gac gga aag ctg ctg gct gca acc ttg ctg ctg	334
Val Arg Ser Ser Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu	
20 25 30	

gca ctg ctg tct tgc ctc acg gtg gtg tct ttc tac cag gtg gcc	382
Ala Leu Leu Ser Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val Ala	
35 40 45	

gcc ctg caa ggg gac ctg gcc agc ctc cgg gca gag ctg cag ggc cac	430
Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His	
50 55 60 65	

cac gcg gag aag ctg cca gca gga gca gga gcc ccc aag gcc ggc ctg	478
His Ala Glu Lys Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly Leu	
70 75 80	

gag gaa gct cca gct gtc acc gcg gga ctg aaa atc ttt gaa cca cca	526
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Glu Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro Pro				
85	90	95		
gct cca gga gaa ggc aac tcc agt cag aac agc aga aat aag cgt gcc				574
Ala Pro Gly Glu Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg Ala				
100	105	110		
gtt cag ggt cca gaa gaa aca gtc actcaa gac tgc ttg caa ctg att				622
Val Gln Gly Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu Ile				
115	120	125		
gca gac agt gaa aca cca act ata caa aaa gga tct tac aca ttt gtt				670
Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe Val				
130	135	140	145	
cca tgg ctt ctc agc ttt aaa agg gga agt gcc cta gaa gaa aaa gag				718
Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys Glu				
150	155	160		
aat aaa ata ttg gtc aaa gaa act ggt tac ttt ttt ata tat ggt cag				766
Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr Gly Gln				
165	170	175		
gtt tta tat act gat aag acc tac gcc atg gga cat cta att cag agg				814
Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln Arg				
180	185	190		
aag aag gtc cat gtc ttt ggg gat gaa ttg agt ctg gtg act ttg ttt				862
Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe				
195	200	205		
cga tgt att caa aat atg cct gaa aca cta ccc aat aat tcc tgc tat				910
Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser Cys Tyr				
210	215	220	225	
tca gct ggc att gca aaa ctg gaa gaa gga gat gaa ctc caa ctt gca				958
Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu Ala				
230	235	240		
ata cca aga gaa aat gca caa ata tca ctg gat gga gat gtc aca ttt				1006
Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp Val Thr Phe				
245	250	255		
ttt ggt gca ttg aaa ctg ctg tgacctactt acaccatgtc tgttagctatt				1057
Phe Gly Ala Leu Lys Leu Leu				

<210> 19
<211> 1430
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (102)...(848)

<400> 19

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	Met Ala Met Ala Phe
	1 5
tgc ccc aaa gat cag tac tgg gac tcc tca agg aaa tcc tgt gtc tcc	164
Cys Pro Lys Asp Gln Tyr Trp Asp Ser Ser Arg Lys Ser Cys Val Ser	
10 15 20	
tgt gca ctg acc tgc agc cag agg agc cag cgc acc tgt aca gac ttc	212
Cys Ala Leu Thr Cys Ser Gln Arg Ser Gln Arg Thr Cys Thr Asp Phe	
25 30 35	
tgc aaa ttc atc aat tgc cga aaa gag caa ggc agg tac tac gac cat	260
Cys Lys Phe Ile Asn Cys Arg Lys Glu Gln Gly Arg Tyr Tyr Asp His	
40 45 50	
ctc ctg ggg gcc tgc gtc agc tgt gac tcc acc tgc aca cag cac cct	308
Leu Leu Gly Ala Cys Val Ser Cys Asp Ser Thr Cys Thr Gln His Pro	
55 60 65	
cag cag tgt gcc cac ttc tgt gag aaa agg ccc aga agc cag gcg aac	356
Gln Gln Cys Ala His Phe Cys Glu Lys Arg Pro Arg Ser Gln Ala Asn	
70 75 80 85	
ctc cag ccc gag ctc ggg aga cca cag gcc ggg gag gtg gaa gtc agg	404
Leu Gln Pro Glu Leu Gly Arg Pro Gln Ala Gly Glu Val Glu Val Arg	
90 95 100	
tca gac aac tca gga agg cac cag gga tct gag cat ggt cca gga ttg	452
Ser Asp Asn Ser Gly Arg His Gln Gly Ser Glu His Gly Pro Gly Leu	
105 110 115	
agg cta agt agc gac cag ctg act ctc tac tgc aca ctg ggg gtc tgc	500

Arg Leu Ser Ser Asp Gln Leu Thr Leu Tyr Cys Thr Leu Gly Val Cys			
120	125	130	
ctc tgc gcc atc ttc tgc tgt ttc ttg gtg gcc ttg gcc tcc ttc ctc			548
Leu Cys Ala Ile Phe Cys Cys Phe Leu Val Ala Leu Ala Ser Phe Leu			
135	140	145	
agg cgt aga gga gag cca cta ccc agc cag cct gcc ggg cca cgt ggg			596
Arg Arg Arg Gly Glu Pro Leu Pro Ser Gln Pro Ala Gly Pro Arg Gly			
150	155	160	165
tca caa gca aac tct ccc cac gcc cac cgc ccc gtg aca gag gct tgc			644
Ser Gln Ala Asn Ser Pro His Ala His Arg Pro Val Thr Glu Ala Cys			
170	175	180	
gac gag gtg acc gcg tca ccc cag cct gtg gaa acg tgt agc ttc tgc			692
Asp Glu Val Thr Ala Ser Pro Gln Pro Val Glu Thr Cys Ser Phe Cys			
185	190	195	
ttc ccg gag cgc agt tct ccc act cag gag agc gcg ccg cgt tcg ctc			740
Phe Pro Glu Arg Ser Ser Pro Thr Gln Glu Ser Ala Pro Arg Ser Leu			
200	205	210	
ggg ata cac ggc ttc gcg ggc act gcc gcc ccg cag ccc tgt atg cgt			788
Gly Ile His Gly Phe Ala Gly Thr Ala Ala Pro Gln Pro Cys Met Arg			
215	220	225	
gca aca gta ggc ggc ctg ggt gtc ctg cgc gca tcc act ggg gac gct			836
Ala Thr Val Gly Gly Leu Gly Val Leu Arg Ala Ser Thr Gly Asp Ala			
230	235	240	245
cgt ccg gca act tgacagccccg aaaaataaaaa aagacaattt agaggatgga			888
Arg Pro Ala Thr			
gtgacagagg gggaaaggga tggagaagag acagatgaag acacgataaa ggaagcccg			948
ctgcacccac gcagagcaac aaagcaacca cctgcagcgc ccacgttccc agcacccgct			1008
gtgcctgccg ctgtgtccta tactttccag agcagtcaac ctgtgccttt tttcttttagt			1068
cgagaaagat ggagaatgac cggcacctag cattaccctt acaaattctta caaacaagtg			1128
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taacttgtat gtgtatgtc agattcgGGG ttatgtcata tgtgcattgt tacgtgagtt			1248
gtgtgtctgt atgagttgtg tgtatatgtg cgccataaaa tatgtgtgt aattctgtgc			1308
atgcagatgt gtgtgtacat atgtgtctgg ctgatgtgg atagccagaa agatgaggGC			1368
ccttcttaggt gaaggccaaa catctaaaaa ccatcttaggt gatgggtgct cgtgccaat			1428
tc			1430

<210> 20
<211> 249
<212> PRT
<213> Mus musculus

<400> 20
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Lys Ser Cys Val Ser Cys Ala Leu Thr Cys Ser Gln Arg Ser Gln Arg
20 25 30
Thr Cys Thr Asp Phe Cys Lys Phe Ile Asn Cys Arg Lys Glu Gln Gly
35 40 45
Arg Tyr Tyr Asp His Leu Leu Gly Ala Cys Val Ser Cys Asp Ser Thr
50 55 60
Cys Thr Gln His Pro Gln Gln Cys Ala His Phe Cys Glu Lys Arg Pro
65 70 75 80
Arg Ser Gln Ala Asn Leu Gln Pro Glu Leu Gly Arg Pro Gln Ala Gly
85 90 95
Glu Val Glu Val Arg Ser Asp Asn Ser Gly Arg His Gln Gly Ser Glu
100 105 110
His Gly Pro Gly Leu Arg Leu Ser Ser Asp Gln Leu Thr Leu Tyr Cys
115 120 125
Thr Leu Gly Val Cys Leu Cys Ala Ile Phe Cys Cys Phe Leu Val Ala
130 135 140
Leu Ala Ser Phe Leu Arg Arg Arg Gly Glu Pro Leu Pro Ser Gln Pro
145 150 155 160
Ala Gly Pro Arg Gly Ser Gln Ala Asn Ser Pro His Ala His Arg Pro
165 170 175
Val Thr Glu Ala Cys Asp Glu Val Thr Ala Ser Pro Gln Pro Val Glu
180 185 190
Thr Cys Ser Phe Cys Phe Pro Glu Arg Ser Ser Pro Thr Gln Glu Ser
195 200 205
Ala Pro Arg Ser Leu Gly Ile His Gly Phe Ala Gly Thr Ala Ala Pro
210 215 220
Gln Pro Cys Met Arg Ala Thr Val Gly Gly Leu Gly Val Leu Arg Ala
225 230 235 240
Ser Thr Gly Asp Ala Arg Pro Ala Thr
245

<210> 21
<211> 473
<212> DNA
<213> Artificial Sequence

<220>

<223> Northern Blot Probe

<400> 21

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ttctgcaggta cactcagctg ccgcaaggag caaggcaagt tctatgacca	tctcctgagg	180
gactgcata gctgtgcctc catctgtgga cagcaccta agcaatgtgc	atacttctgt	240
gagaacaagc tcaggagccc agtgaacctt ccaccagagc tcaggagaca	gcggagtggaa	300
gaagttgaaa acaattcaga caactcggga agttaccaag gattggagca	cagaggctca	360
gaagcaagtc cagctctccc ggggctgaag ctgagtgac atcaggtggc	cctggtctac	420
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<210> 22

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> ZC20061

<400> 22

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<210> 23

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC20062

<400> 23

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<210> 24

<211> 256

<212> DNA

<213> Artificial Sequence

<220>

<223> Northern Blot probe

<400> 24

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<400> 28
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<210> 29
<211> 17
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<223> Oligonucleotide ZC24198

<400> 29
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<210> 30
<211> 16
<212> DNA
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<220>
<223> Oligonucleotide ZC24199

<400> 30
gcacaagtgg ggtcgg 16

<210> 31
<211> 19
<212> DNA
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<220>
<223> Oligonucleotide ZC24271

<400> 31
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<210> 32
<211> 17
<212> DNA
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<220>
<223> Oligonucleotide ZC24272

<400> 32	
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<210> 33	
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<223> Oligonucleotide ZC24495	
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<400> 34	
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<213> Homo sapiens	
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aagttcaagt agtatatgg atgactccac agaaaaggag cagtcacgcc ttacttcttg	180
ccttaagaaa agagaagaaa tgaaactgaa ggagtgtgtt tccatcctcc cacggaagga	240
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tcagggtcca gaagaaacag tcactcaaga ctgcttgc当地 ctgattgcag acagtgaaac	600
accaactata caaaaaggat cttacacatt tggccatgg cttctcagct taaaagggg	660
aagtgcccta gaagaaaaag agaataaaaat attggtcaaa gaaactggtt acttttttat	720
atatggtcag gtttatata ctgataagac ctacgccatg ggacatctaa ttcagaggaa	780
gaaggtccat gtcttgggg atgaattttag tctggtgact ttgtttcgat gtattcaaaa	840

tatgcctgaa acactaccca ataattcctg ctattcagct ggcattgcaa aactggaaga	900
aggagatgaa ctccaaacctt caataccaaag agaaaaatgca caaatatcac tggatggaga	960
tgtcacattt tttggtgcat tgaaaactgct gtgacctact tacaccatgt ctgttagctat	1020
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aaaaaaaaaa	1090
<210> 36	
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<400> 37	
gtatacggcg cgccctcacag cagtttcaat gc	32
<210> 38	
<211> 25	
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<223> Oligonucleotide ZC17251	
<400> 38	
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<210> 39	
<211> 25	
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<223> Oligonucleotide ZC17252

<400> 39

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<210> 40

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC17156

<400> 40

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<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC17157

<400> 41

cttttgctag cctcaaccct gactatc 27

<210> 42

<211> 813

<212> DNA

<213> Homo sapiens

<400> 42

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cccgggcggag	gagtgtgtt	ccgagtggga	ctgcatgtgt	gtccagcctg	aattccactg	240
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gaccctggctg	ctgctggagg	tgccgcccgtc	gaccgaagac	gccagaagct	gccagttccc	660
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1	5	10	
aga tgg gtc ctg tcc gag ccc aga tct tca gac aaa act cac aca tgc Arg Trp Val Leu Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys	96		
15	20	25	30

cca ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu 35 40 45	144
ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cg ^g acc cct gag Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu 50 55 60	192
gtc aca tgc gtg gtg gac gtg agc cac gaa gac cct gag gtc aag Val Thr Cys Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys 65 70 75	240
ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys 80 85 90	288
ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu 95 100 105 110	336
acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys 115 120 125	384
gtc tcc aac aaa gcc ctc cca tcc atc gag aaa acc atc tcc aaa Val Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys 130 135 140	432
gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc Ala Lys Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser 145 150 155	480
cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys 160 165 170	528
ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln 175 180 185 190	576
ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly 195 200 205	624
tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag	672

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 210 215 220

cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac 720
 Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 225 230 235

cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa taatctaga 768
 His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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 Ile Pro Arg Glu
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Val Lys Glu Thr
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